Ubiquitin-Specific Protease 2

Alternative Names
USP2
Ubiquitin-Specific Protease, 41-KD
UBP41

Record Category
Gene locus

WHO-ICD
N/A to gene loci

Incidence per 100,000 Live Births
N/A to gene loci

OMIM Number
604725

Mode of Inheritance
N/A to gene loci

Gene Map Locus
11q23.3

Description
Ubiquitination is a cellular process by which a small regulatory protein called ubiquitin is attached to a substrate protein. This protein modification can target the substrate for degradation through the proteasome, alter its cellular location, affect its activity or promote/prevent protein interactions. The subsequent disassembly of polyubiquitin chains and release of ubiquitin from the degraded protein, a process known as deubiquitination, is carried out by ubiquitin-specific proteases such as USP2.

USP2 belongs to the peptidase C19 superfamily and targets polyubiquitinated proteins such as MDM2, MDM4 and cyclin D1. As MDM2 and MDM4 are negative regulators of the p53 tumor suppressor, USP2 indirectly promotes p53/TP53 degradation and limits p53 activity. Through cyclin D1, USP2 plays a role in the G1/S cell-cycle progression in normal and cancer cells. The protein is also involved in the biological processes of circadian behavior, locomotor rhythm and regulation of skeletal muscle tissue development.

Molecular Genetics
The USP2 gene is located on the long arm of chromosome 11 at position 11q23.3. It spans a length of 26.5 kb and its coding sequence is spread across 17 exons. The protein product encoded by USP2 has a molecular mass of 68 kDa and consists of 605 amino acids. Alternatively spliced transcript variants encode multiple isoforms of the USP2 protein. The gene is found to be overexpressed in the heart, skeletal muscle and testis.

Epidemiology in the Arab World
Saudi Arabia
Anazi et al. (2016) determined the effectiveness of genomic tools in diagnosing Intellectual Disability (ID) cases. The authors carried out molecular karyotyping, exome sequencing and sequencing by a neurological gene panel on 337 ID patients. Genomic tools were found to have a higher diagnostic yield than standard clinical evaluations (58% vs 16%). In a 2.5 year old boy suffering from global developmental delay, hypotonia, bilateral talipo-equinovarus deformity, seizures, cryptorchidism and brain abnormalities, exome sequencing helped uncover a homozygous c.550G>A (p.Gly184Arg) mutation in the USP2 gene. The amino acid change occurred in the N-terminal region and was predicted to affect subcellular localization and binding to other proteins.

References
Anazi S, Maddirevula S, Faqeih E, Alsedairy H, Alzahrani F, Shamseldin HE, Patel N, Hashem M, Ibrahim N, Abdulwahab F, Ewida N, Alsaif HS, Al Sharif H, Alamoudi W, Kentab A, Bashiri FA, Alnaser M, AlWadei AH, Alfadhel M, Eyaid W, Hashem A, Al Asmari A, Saleh MM, AlSaman A, Alhasan KA, Alsughayir M, Al Shammari M, Mahmoud A, Al-Hassnan ZN, Al-Husain M, Osama Khalil R, Abd El Meguid N, Masri A, Ali R, Ben-Omran T, El Fishway P, Hashish A, Ercan Sencicek A, State M, Alazami AM, Salih MA, Altassan N, Arold ST, Abouelhoda M, Wakil SM, Monies D, Shaheen R, Alkuraya FS. Clinical genomics expands the morbid genome of

intellectual disability and offers a high diagnostic yield. Mol Psychiatry. 2016 Jul 19. PMID: 27431290.

Related CTGA Records

External Links

http://www.genecards.org/cgi-bin/carddisp.pl?gene=USP2

Contributors

Sayeeda Hana
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